Amendments to the claims

This listing of claims will replace all prior versions and listings of claims in the application.

Listing of Claims:

1. (Currently Amended) A process for synthesizing a nucleic acid complementary to a target nucleic acid sequence in a template nucleic acid, which comprises the steps of:
(a) annealing a primer to said template nucleic acid and synthesizing a complementary nucleic acid comprising the complementary sequence of said target nucleic acid sequence by a primer extension reaction,

wherein the primer comprises in its 3'-end portion a sequence (Ac') that hybridizes to a sequence (A) in the 3'-end portion of the target nucleic acid sequence, and in the 5'-side of said sequence (Ac'), a sequence (B') that hybridizes to the complementary sequence (Bc) of a sequence (B) positioned in the 5'-side of said sequence (A) on the target nucleic acid sequence,

wherein in the absence of an intervening sequence between said sequences (Ac') and (B'), X is in the range of 10 to 30, (X - Y)/X is in the range of -1.00 to 0.75, and (X+Y) is in the range of 30 to 50, in which X denotes the number of bases in said sequence (Ac'), and Y denotes the number of bases in a region flanked by said sequences (A) and (B) on the target nucleic acid sequence, and

wherein in the presence of an intervening sequence between said sequences (Ac') and (B'), X is in the range of 10 to 30,{X - (Y - Y')}/X is in the range of -1.00 to 0.75, and (X+Y+Y') is in the range of 30 to 50, in which X and Y have the same meanings as above, and Y' denotes the number of bases in said intervening sequence;
(b) hybridizing the sequence (B') positioned in the 5'-side of the complementary nucleic acid synthesized in step (a) with the sequence (Bc) on the same complementary nucleic acid, thereby allowing the portion of said sequence (A) on the template nucleic acid to be single-stranded, and
(c) annealing another primer having the same sequence as said primer to the single-stranded sequence (A) portion of the template nucleic acid from step (b) and conducting strand displacement reaction, thereby displacing the complementary nucleic acid synthesized in step (a) by the complementary nucleic acid newly synthesized with said another primer, and steps (a), (b) and (c) are carried out in an isothermal condition.

2. (Previously presented) The process according to claim 1, wherein the double-stranded nucleic acid obtained by step (c) is used repeatedly in step (b).

3. (Currently Amended) The process according to claim 1, wherein steps (a), (b) and (c) are carried out in an isothermal condition using a primer with a strand length of 15 to 100 nucleotides.

4. (Original) The process according to claim 1, wherein a DNA polymerase having strand displacement ability is used.

5. (Original) The process according to claim 1, further comprising a step of synthesizing cDNA with a reverse transcriptase when the template nucleic acid is RNA.

6. (Previously presented) The process according to claim 1, wherein steps (a), (b) and (c) are carried out in the presence of a melting temperature adjusting agent.

7. (Previously presented) The process according to claim 6, wherein the melting temperature adjusting agent is dimethyl sulfoxide, betaine, formamide or glycerol, or a mixture thereof.

8. (Original) The process according to claim 1, wherein the target nucleic acid sequence in the template nucleic acid comprises non-natural nucleotide(s).

9. (Currently Amended) A process for amplifying a target nucleic acid sequence in a double-stranded template nucleic acid, which comprises the steps of:
(a) annealing first and second primers to first and second template nucleic acids of a double-stranded template nucleic acid, respectively, and synthesizing first and second complementary nucleic acids comprising the complementary sequence of said target nucleic acid by a primer extension reaction, respectively,

wherein the first primer comprises in its 3'-end portion a sequence (Ac') that hybridizes to a sequence (A) in the 3'-end portion of the target nucleic acid sequence in the first strand of the double-stranded template nucleic acid, and in the 5'-side of said sequence (Ac') a sequence (B') that hybridizes to the complementary sequence (Bc) of a sequence (B) positioned in the 5'-side of said sequence (A) on said target nucleic acid sequence,

wherein in the absence of an intervening sequence between said sequences (Ac') and (B'), X is in the range of 10 to 30, (X - Y)/X is in the range of -1.00 to 0.75, and (X+Y) is in the range of 30 to 50, in which X denotes the number of bases in said sequence (Ac'), and Y denotes the number of bases in a first region flanked by said sequences (A) and (B) on the target nucleic acid sequence,

wherein in the presence of an intervening sequence between said sequences (Ac') and (B'), X is in the range of 10 to 30, {X - (Y - Y')}/X is in the range of -1.00 to 0.75, and (X+Y+Y') is in the range of 30 to 50, in which X and Y have the same meanings as above, and Y' denotes the number of bases in said intervening sequence,

wherein the second primer comprises in its 3'-end portion a sequence (Cc') that hybridizes to a sequence (C) in the 3'-end portion of the target nucleic acid sequence in the second strand of the double-stranded template nucleic acid, and in the 5'-side of said sequence (Cc') a sequence (D') that hybridizes to the complementary sequence (Dc) of a sequence (D) positioned in the 5'-side of said sequence (C) on said target nucleic acid sequence,

wherein in the absence of an intervening sequence between said sequences (Cc') and (D'), X is in the range of 10 to 30, (X - Y)/X is in the range of -1.00 to 0.75, and (X+Y) is in the range of 30 to 50, in which X denotes the number of bases in said sequence (Cc'), and Y denotes the number of bases in a second region flanked by said sequences (C) and (D) on the target nucleic acid sequence, and

wherein in the presence of an intervening sequence between said sequences (Cc') and (D'), X is in the range of 10 to 30, {X - (Y - Y')}/X is in the range of -1.00 to 0.75, and (X+Y+Y') is in the range of 30 to 50, in which X and Y have the same meanings as above, and Y' denotes the number of bases in said intervening sequence;

(b) hybridizing the sequences (B') and (D') positioned in the 5'-side of the first and second complementary nucleic acids synthesized in step (a) with the sequences (Bc) and (Dc) on the same complementary nucleic acid, respectively, and thereby changing the portions of said

sequences (A) and (C) on the first and second template nucleic acids into a single strand, respectively, and

(c) annealing additional primers having the same sequence as said primers to the single-stranded sequence (A) and (C) portions of the first and second template nucleic acids from step (b) and conducting strand displacement reaction, thereby displacing the first and second complementary nucleic acids synthesized in step (a) by the complementary nucleic acids newly synthesized with said additional primers, and

steps (a), (b) and (c) are carried out in an isothermal condition.

10. (Previously presented) The process according to claim 9, wherein the double-stranded nucleic acids obtained by step (c) are used repeatedly in step (b).

11. (Previously presented) The process according to claim 9, wherein the first and second complementary nucleic acids obtained as single strands by step (c) are used repeatedly as the second and first template nucleic acids, respectively, in step (a).

12. (Previously presented) The process according to claim 9, wherein steps (a), (b) and (c) are carried out in an isothermal condition.

13. (Original) The process according to claim 9, wherein a DNA polymerase having strand displacement ability is used.

14. (Original) The process according to claim 9, further comprising a step of synthesizing cDNA with a reverse transcriptase when the template nucleic acid is RNA.

15. (Previously presented) The process according to claim 9, wherein steps (a), (b) and (c) are carried out in the presence of a melting temperature adjusting agent.

16. (Previously presented) The process according to claim 15, wherein the melting temperature adjusting agent is dimethyl sulfoxide, betaine, formamide or glycerol, or a mixture thereof.

17. (Previously presented) The process according to claim 9, wherein the target nucleic acid sequence in the double-stranded template nucleic acid comprises non-natural nucleotide(s).

18-23. (Canceled)